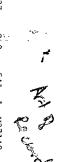
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 08:01:01 2000; MasPar time 23.59 Seconds 668.825 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Scoring table: PAM 150 Gap 11 >US-09-331-631-1 (1-666) from US09331631.pep (1 of 5) 4924 1 MAINTSNLCSLLFLLSLFLL......SPRSTKQQQPLVSILDFVGF 666

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 37.170; Variance 173.030; scale 0.215

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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17 18 19	112 15 15	10087654321	Result.
1559 1460	930 924 917 883 883	4924 4746 47467 1330 1246 1178 1178 1109 1063 1026	Score
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			DB
W03474 R60054 W88788 W31867	W62838 W90342 W22150 W22149 W62834	W62839 W62839 W62830 R20181 W62833 W62833 W62833 W62831 W62831 W62835 W90341	Ħ
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## ALIGNMENTS

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22-DEC-1997; AU0874.

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BOWET NI, Goulter KC, Green JL, M.

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The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
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1 Bower NI, Goulter "KC, Green JL, Manners JM, Marcus R WPI; 98-377279/32.
N N-PSDB; V42316.
PT Novel anti-microbial protein from e.g. Macadamia useful for cohtrolling microbial infestations of PS Claim 1; Page 43-45; 96pp: English.
CC The sequence is that of an antimicrobial proteir has used to control microbial infestations in plants.
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WPI; 92-024418/03.
N-PSDB; Q20377.
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The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close the 47 kD and 31 kD polypeptides.
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(RETR-) COULTER KC, Green JL, Manners JM, Mar
BOWET NI, Goulter KC, Green JL, Manners JM, Mar
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The sequence is that of an antimicrobial protein which compared to control microbial infestations in plants and
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VEESFNSQDQSIFFPGPRQHQQQS 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEADVEMACPHL---SG--RHGGRGGGKRHEEEED--V-HYEQVRARLSKREAIVVLAGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEATSPRE----KSGE--RFAFN | ::| | :| | ::| | ::| | ::| | ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGTTEYLINRDNNERLHIAKELQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGSTVYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRY-EKEK--R-K-Q--QKRYEE-QQ--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPPKRYEDCRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVFVSSGNENLLLFAFGINAQN-N--H-EN-FLAGRERNVLQQIEPQAMELAFAAPRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                            525 AA;
                                                                                                                23.9%;
ilarity 40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525
                                                                                                               Score 1178; DB 1;
Pred. No. 3.05e-92;
125; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                 .g. Macadamia integrifolia festations of plants or man
                                                                                                                                                                                                                                                                                                                                                                                                        control
                                                                                                                                                                                                                                                                                                  JM, Marcus JP;
                                                                                                                                             Length
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Matches
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02-JUL-1998.
02-JUL-1998.
22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, Mar
MPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1, Page 58-60; 96pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
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Zea mays antimicrobial pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W62835;
27-OCT-1998
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     415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 22.3%;
Local Similarity 40.4%;
les 202; Conservative
                                                                                                                                                                                                                                                                                                                                                           84
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EDDNHHHHGGHKSGQCVRRCEDR-PWHQRPRCLEQCREEEREKRQERSRHEADDRSGEGS
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                                                                                                                                                                                                         EANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINR
                                                                                                                                                                                                                                                                                                            GRYE-EGEEE-QSDN-PYYFDERSLSTRERTEEGHISVLENFYGRSKLLRALKNYRLVLL
                                                                                                                                                                                                                                                                                                                                      SEDEREQEKEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYRVAVL 143
                                                                                                                                                                                                                                                                                                                                                                                                              AFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESE: | | ::: | :| :| :| :| :| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPEQIRAISQQATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVS
  QQ-RE-GVIIRASQEQIRELTRDDSES-R--HWHIRRGGESSRGPYNLFNKRPLYSNKYG
                                                                                                    DNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFG
                                                                                                                                  DGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLERLFG
                                                                                                                                                                                                                                                      EANPRSFYVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDV--HYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 AA;
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infestation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.41e-85;
113; Mismatches 156;
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plants or man
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a novel sucrose binding protein, SBP2 isolated CF from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a CF modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers CF cand where expression of the modified SBP in a yeast assay system confers CF confided sucrose uptake compared to the corresponding wild-type SBP. CF the products of the invention can be used for producing transgenic plants CF which have modified sucrose uptake activity, particularly in developing compared to the seed sucrose uptake activity in developing seeds may be CF consistent which have modified sucrose uptake activity in developing seeds. Enhanced sucrose uptake activity in developing seeds may be CF the seed (e.g. where the seed is the primary plant material harvested, CF the seed (e.g. where the seed is the primary plant material harvested, CF sucrose suptake activity in the plant is confirm the desirable where the vegetative material of the plant is confirm seeds.
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds Claim 13b; Page 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chao WS, Grimes HD; WPI; 99-070155/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SBP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W90341 standard;
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(UNIW ) UNIV WASHINGTON STATE RES
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21-MAY-1998; U10465
                                                                                                                                                                                                                                                                                                                                                                                                                          transgene in developing
366 LQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636
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                                                                                                                                                                                                                                                                                                                        / Match 21.6%;
Local Similarity 36.2%;
nes 169; Conservative
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                                       HIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFNQQNEGSIFKIS
                                                                           HFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDENEKLLLAML 213
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                                                                                                                                                           QSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT 305
                                                                                                                                                                                EDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFPGPRQHQQQSPRSTKQQQ 655
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                                                                                                                                                                                                                                        QQREYEDCRRRCEQQ-E-P-RQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEE
                                                                                                                                                                                                                                                                                EDPELVTCKHQCQQQRQYTESDKRTCLQQCDSMKQEREKQVEEETREKEEEHQ-EQHEEE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLPGPEESGGHEEREQEEEE 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sucrose binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                       489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 489
                                                                                                                                                                                                                                                                                                                                                                                                                          seeds.
                                                                                                                                                                                                                                                                                                                      Score 1063; DB 1; 1
Pred. No. 7.99e-82;
137; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EDV-H-YEQVRARLSKREAIVVLAGHPVVFVSS
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified plant sucrose binding
transgenic plants which can have en
uptake activity in developing seeds
Disclosure; Page 34-36; 58pp; Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chao WS, Grimes HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND
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                                                                                             308
                                                                                                                                                     167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            max SBP1
QQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQ-EETRE-KKEEEESREREEEQQEQHEEQD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGKRHEEE 544
                                                                                                                                                                                                                 DNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHL
                                                                                                                                                                                                                                                QQREY-EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPS-YHRISADLKPGMVFVVPPGHPFVTIASNKENLLIICFEVNVRDNK-KFTFAGKD-N 441
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24 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1026; DB 1;
Pred. No. 1.77e-78;
120; Mismatches 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PT uptake activity in developing seeds
PS Claim 7; Page 36-37; SBpp; English.

CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC such as Soybean. In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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21-MAY-1998; U10465.
21-MAY-1997; US-047568.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max.
WO9853086-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seed; carbohydrate content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G. max truncated SBP1 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 10
W90340 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.6%;
Local Similarity 38.8%;
Nes 158; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                               DSEVVEFNIKGRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVNRDENDKLFLAMLHI 226
                                                                                                                                                                                                                                                       ENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPRHF 166
                                                                                                                                                                                                                                                                                                                                                                                                                        QQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQ-EETRE-KKEEEESREREEEQQEQHEEQD 106
PVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQAALQTPKGKLENVFDQQNEGSIFRIS 286
                                                                                DADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF-L 366
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                                                                                                                                                                                                                    DNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHL
                                                                                                                                                                                                                                                                                                                                                         QQREY-EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQS 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVLQQIEPQAMELAFAAPRKEVEESF 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIVSSLDNVAKELAFNYPSEMVNGVF 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENF-LAGRER 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developing seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 964; DB 1;
pred. No. 6.98e-73;
109; Mismatches 123
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Best Local
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22-DEC-1997;
20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 63-65 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPIC
Bower NI, Goulter KC, Green
WPI; 98-377279/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max antimicrobial protein. antimicrobial protein; infestation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animals.
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                                                                                                                  GQNPEPYLSTFSKEILEAALNTQ-TE--K-L--R--GVF-GQQR--EGVIIRASQEQIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q-TISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRAS
   IANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEEDVHYE
                                                                           LSKRAKSSSRK-TI--SSED-K-PFNLRSRDPIYSNKLGKFFEITPEKNPQLRDLDIFLS
                                                                                                                                                                        KMIHHINRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAG
                                                                                                                                                                                                                                                                                                                           DERQFPFPRPPHQKEERNEEEDEDE-EQQRESEES-EDSELRRHKNKNPFLFGSNRFETL
                                                                                                                                                                                                                                                                                                                                                                           EDEDE-QPR-PIPFPRPQPR-QEEEHEQREE-QEWPRKEE-KRGEKGSEEED-EDEDEEQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRCROQESGPROQQYCQRRCKEICEEEEEYNRQRDPQQQYEQCQKHCQRRETEPRHMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLQSCNSERDSYRNQA-CHARCNLLKVEKEECEEGEIPRPR-PRPQ-HPEREPQQPGEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQVRALAPIKKSSW-WPF--GGES-KPQFNIFSKRPIISNGYGRLIEVGPDDDEKSWLQ
                              IVDMNEGALLLPHFNSKAIVILVINEGDANIELV-G-LKEQQ--QE---QQQEEQPLEVR
                                                          LT-RDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVF
                                                                                                                                              TEAQQSYLOGFSRNILEASYDTKFEEINKVLFSREEGQQQGEQRLQESVIVEISKEQIRA
                                                                                                                                                                                                          SLVNNDDRDSYRLQSGDALRVPSGTTYYVVNPDNNENLRLITLAIPVNKPGRFESFFLSS
                                                                                                                                                                                                                                       FRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGAL
                                                                                                                                                                                                                                                     EPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGE-EEQSD-NPYYFDERSLSTR
                                                                                                                                                                                                                                                                                                                                                           TCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMDLSVFIANVTQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRGGGKRHEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEQIRELTRODSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDY-RQ-LQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSPS-YHRISSDLKPGMVFVVPPGHPFVTIASNKENLLMICFEVNAR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 18.9%;
Similarity 32.7%;
193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 930; DB 1;
Pred. No. 8.08e-70;
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RESULT WEST CONSTRUCTION OF STREET O
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PT transgenic plants which can have enhanced or decreased sucrose

PT uptake activity in developing seeds

Claim 7; Page 39-40; Sbpp; English.

CC This sequence represents a novel sucrose binding protein, SBP2 isolated

CC from Glycine max. This protein is used in a method resulting in the

production of a modified plant sucrose binding protein (SBP) which has a

CC modified amino acid sequence compared to a corresponding wild-type SBP.

CC enhanced sucrose uptake compared to the corresponding wild-type SBP.

CC enhanced sucrose uptake compared to the producing transgenic plants

CC which have modified sucrose uptake activity, particularly in developing

CC seeds. Enhanced sucrose uptake activity in developing seeds may be

CC desirable where it is an advantage to increase the carbohydrate content

CC such as soybean). In contrast, decreased sucrose uptake activity in

CC seeds might be desirable where the vegetative material of the plant is

CC harvested. The SBP regulatory regions confer specific or enhanced

CC transgene in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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W90342 standard;
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21-MAY-1998; U10465.
22-MAY-1997; US-047568
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P1; sucrose binding protein; SBP2;
ed; carbohydrate content; soybean.
EDPELVTCKHQCQQQRQYTESDKRTCLQQCDSMKQEREKQVEEETREKEEEHQ-EQHEEE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSIL
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                                                                                                            QEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQD
                                                                                                                                             RERVRALAPIKKSSW-WPF--GGES-KAQFNIFSKRPIFSNGYGRLIEVGPDDEKSWLQR
                                                                                                                                                                                                                                              LQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRAS
                                                                                                                                                                                                                                                                                           HIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLENQQNEGSIFKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPR 153
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Pred. No. 2.80e-69;
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Best Local :
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23-SEP-1996; U15222.
04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
(UYAR-) UNIV ARKANSAS.
Bannon GA, Burks AW, Co
WPI; 97-363453/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide comprises major peanut allergen Ara hI (W22149). Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W22150 standard; Protein; W22150; 
29-DEC-1997 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peanut allergens Ara hI and Ara hII -
two-site monoclonal antibody based EL.
Claim 31; Page 172; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; anaphylactic shock; immunotherapy monoclonal antibody; ELISA; analysis; Ara Arachis hypogaea strain Florunger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines to protect against allergic reactions to peanut allergens. e.g. anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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  ALNTQTEKLRGVF-----GQQRE-GVI---IRASQE-Q--IRELTRDD-SE-SRH-WHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQRRCKEICEEEEEYNRQRDPQQQYEQCQKHCQRRETEPR-HMQTCQQRCERRYEKEKRK 160
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                                                  AFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSV
                                                                                                                                                             LRIPSGFISYILNRHDNQNLRVAKISMPVTQPGQFEDFFPASSRDQSSYLQGFSRNTLEA
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                                                                                                          IRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEA
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                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                      two-site monoclonal antibody based ELISA

Claim 31; Page 169; 354pp; English.

This polypeptide comprises major peanut allergen Ara HI (W22149).

CIts sequence was deduced from cDNA clone P17 (T76612), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara HI peptide (see w24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum CIF from a large proportion of individuals with peanut the hypersensitivity. Ara HI and Ara HII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site can be considered and the service of the detection of Ara HI or Ara HII (claimed). IgE-contained to protect against allergic reactions to peanut allergens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1996; U15222.

04-MAR-1996; US-610424.

29-DEC-1995; US-009455.

(UYAR-) UNIV ARKANSAS.

Bannon GA, Burks AW, Cockrell G,

WPI; 97-363453/33.
                                                                                                                                                                                                                                                                                                                                                                                   e.g. anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T76612.
Peanut allergens Ara hI and Ara hII - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9724139-A1.
10-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monocional antibody; ELISA; analysis; Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W22149 standard;
W22149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arachis hypogaea strain Florunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peanut allergen Ara hI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1997
                                                            105
                                                                                                                      119
176 YEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRG
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                                                                                                                                                                                45
                                                                                                                                                                                                                                       Local Similarity es 192; Conser
                                    EGGRWGPAEP-RE-RERE-ED-WRQPREDWRRPSHQ-QPR-KI--RPEGREGE---QEWG 153
                                                                                                                                                                       QQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDDRRQPRRE 104
                                                                                                                   QRDPQQQYEQ-CQKHCQRRETEPRHMQTCQQRCERRYEKEK-R-KQQKRYEEQQREDEEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQP
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                                                                                                                                                                                                                                                               17.9%;
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                                                                                                                                                                                                                                 Score 883; DB 1; Length 614
Pred. No. 1.37e-65;
158; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanley JS;
                                                                                                                                                                                                                                                                                              Length 614,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         656
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                                                                                                                                                                                                                                                                                                                                                                                                                  peanut allergens,
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                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPIC.
BOWER NI, GOULTER KC, Green
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                         Novel anti-microbial protein from e.g. Macadamia integrifo useful for controlling microbial infestations of plants or Claim 1; Page, 55-57; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arachis hypogaea antimicrobial prote antimicrobial protein; infestation;
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                               animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arachis hypogaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W62834;
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                                                                                                                      176
                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630
                   213
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                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                           Local
                                                                     TPGS-EVREETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQIE
                                                                                                                                        EGGRWGPAEP-RE-RERE-ED-WRQPREDWRRPSHQ-QPR-KI--RPEGREGE---QEWG
               ARPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRH
                                                     GSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLE
                                                                                                                                                                                        QRDPQQQYEQ-CQKHCQRRETEPRHMQTCQQRCERRYEKEK-R-KQQKRYEEQQREDEEK
                                                                                                                                                                                                                        QQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDDRRQPRRE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQRES-HFVSARPQSQSPSSPEKEDQ
                                                                                                                     YEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQDQSIFFPGPRQHQQQSPRSTKQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GQQRE-GVI---IRASQEQ--IRELTRDDS-E-SRH-WHI-RRGGES-S-RGPYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNQNLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEADVEMACPHLSGRHGGRGGGKRHEEEEEDVHYE----QVR---ARLSKREAIVVLAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGNLELVAVRKEQQQRGRREQEWEEEEEEDEEEEGSNREVRRYTARLKEGDVFIMPAAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNKRPLYSNKYGQAYEVKPED-YRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDGEPDLSNNFGRLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF--
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                                                                                                                                                                                                                                                        ch 17.9%;
l Similarity 33.9%;
192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                               614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TROPICAL PLANT PATHOLOGY.

Green JL, Manners JM, Marcus JP;
                                                                                                                                                                                                                                                           158;
                                                                                                                                                                                                                                                        Score 883; DB 1; Le
Pred. No. 1.37e-65;
L58; Mismatches 172;
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                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                               integrifolia
plants or man
                                                                                                                                                                                                                                                           Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                                                mammals
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                        175
                                                                                     212
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